

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2005, 12:32:47 ; Search time 0.001 Seconds  
(without alignments)  
626.560 Million cell updates/sec

Title: US-10-035-958-60

Perfect score: 890  
Sequence: 1 AAGTACTGTGTCTCGGCTGG.....TAAAAAAAAAAATCATCAAA 890

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 0.5

Searched: 1 seqs, 352 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Database: kol035rge\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	330.5	37.1	352	1	G27363

#### ALIGNMENTS

RESULT 1  
G27363/c  
LOCUS: G27363 352 bp DNA linear STS 28-JUN-1996  
DEFINITION human STS SHGC-31033, sequence tagged site.  
ACCESSION G27363  
VERSION G27363.1 GI:1396086  
KEYWORDS STS; STS sequence; primer; sequence tagged site.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 352)  
Myers,R.M.  
Unpublished (1996)

REFERENCE  
AUTHORS  
JOURNAL  
COMMENT

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Primer A: TTGAAAGAGAGGGTCTG  
Primer B: AAGCAAAACCAAGGCG  
STS size: 133  
PCR profile:

Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600

Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/uL  
Total Vol: 10 uL

Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from H83927  
-- Washington University/Merck EST sequence.

FEATURES  
source  
Location/Qualifiers  
1..352  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/map="8"  
STS  
primer\_bind  
4..136  
primer\_bind  
complement(119..136)

Query Match 37.1%; Score 330.5; DB 1; Length 352;  
Best Local Similarity 98.0%; Pred No. 0;  
Matches 344; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY	521	AGTGGCTTCATCGCTACAGTCTTGTCTATCTTCAGAGAAAGTCACTCTCTC	580
DB	352	AGTGGCTTCATCGCTACAGTCTTGTCTATCTTCAGAGAAAGTCACTCTCTC	293
QY	581	CTTCCCAAGAAACAAACTGAGGCTCTTGGAATGACAGATTTCTGAACCTCTC	640
DB	292	CTTCCCAAGAAACAAACTGAGGCTCTTGGAATGACAGATTTCTGAACCTCTC	233
QY	641	CACCTGGGGAACCTGAGCAAGCAACCGATTCATGACCCAGACTACAGACTCACA	700
DB	232	CACCTGGGGAACCTGAGCAAGCAACCGATTCATGACCCAGACTACAGACTCACA	173
QY	701	ACCTTCAGAGCTCCAGAGAGGCGCAGCGCAAGCAC-AAAACGAGCAGAGATA	759
DB	172	ACCTTCAGAGCTCCAGAGAGGCGCAGCGCAAGCACAAAACGAGCGAGATA	113
QY	760	GCTGCTCTGATATGCGGCTTTGCCATCCGGGATGTGGCACAATGCTACCAACGA	819
DB	112	GCTGCTCTGATATGCGGCTTTGCCATCCGGGATGTGGCACAATGCTACCAACGA	53
QY	820	CGATGGGATGAGAACCCCTCTGATACGAACCCCTCTTTTCAAT	870
DB	52	CGATGGGATGAGAACCCCTCTGATACGAACCCCTCTTTTCAAT	2

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